



Were the main mountain ranges in the Korean Peninsula a glacial refugium for plants? Insights from the congeneric pair *Lilium cernuum* – *Lilium amabile*



Mi Yoon Chung^a, Myong Gi Chung^{a,*}, Jordi López-Pujol^b, Ming-Xun Ren^c, Zhi-Yong Zhang^d, Seon Joo Park^e

^a Department of Biology and the Research Institute of Natural Science, Gyeongsang National University, Jinju 660-701, Republic of Korea

^b BioC-GReB, Laboratori de Botànica, Facultat de Farmàcia, Universitat de Barcelona, Barcelona 08028, Spain

^c Key Laboratory of Aquatic Botany and Watershed Ecology, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, Hubei, China

^d Laboratory of Subtropical Biodiversity, Jiangxi Agricultural University, Nanchang 330045, Jiangxi, China

^e Department of Life Science, Yeungnam University, Gyeongsan 712-749, Republic of Korea

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ABSTRACT

The main Korean mountain range (the so-called “Baekdudaegan”), which stretches from north to south across most of the country, has been thought to harbor glacial refugia for boreal plant species, where they likely found relatively stable habitats and maintained large population sizes. Under this scenario, high levels of genetic variation and low or moderate degree of differentiation among populations within these species were expected. To test this hypothesis, we examined levels of allozyme diversity (14 loci) in eight populations of the boreal herb *Lilium cernuum*, which in Korea occurs largely along the Baekdudaegan and, as a reference, in eight populations of its congener *Lilium amabile*, a temperate species that is distributed on lower hillsides in peripheral regions of the Baekdudaegan. *L. cernuum* harbored higher levels of genetic variation within populations than *L. amabile* (%*P* = 49.1 vs. 25.0, *A* = 1.71 vs. 1.34, and *H_e* = 0.159 vs. 0.048). Genetic differentiation among populations was low for both species (*F_{ST}* = 0.119 and 0.014 for *L. cernuum* and *L. amabile*, respectively). A series of historical and ecological factors may explain the contrasting levels of genetic diversity between *L. cernuum* and *L. amabile*: occurrence within the main ranges of the Baekdudaegan (enduring the glacial periods in macrorefugia) vs. low elevation peripheral areas (in microrefugia) and shade-tolerant vs. shade-intolerant. This study, as well as previous population genetics studies, strongly suggests that the Baekdudaegan merits high priority for conservation given its proposed role as glacial refugia for montane species.

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1. Introduction

It is generally thought that the Quaternary glacial-interglacial oscillations played an important role in shaping the current distribution of plant species and, thus, the amount and distribution of genetic diversity within and between populations (Hewitt, 1996, 2004; Hu et al., 2009). High levels of genetic diversity are expected for those areas that are thought to be

* Corresponding author. Tel.: +82 55 772 1343; fax: +82 55 772 1349.

E-mail addresses: mgchung@nongae.gsnu.ac.kr, mgchung@gnu.ac.kr (M.G. Chung).

refugial, as plants would have endured the most adverse periods maintaining relative large populations. Mountainous regions are among the best candidates to harbor glacial refugia throughout the world because of two main reasons. First, they enjoyed a relatively eco-climatic stability along the Quaternary climatic cycles, due to the continued moisture availability (i.e., orographic rainfall) and varied topography (with many sites facing south and west) which would have provided many sheltered habitats from the cold winds (Fjelds  and Lovett, 1997; Tzedakis et al., 2002; Kaltenrieder et al., 2009; M dail and Diadema, 2009). Second, because an altitudinal retreat of only 10 m might be equivalent to a ca. 10-km latitudinal retreat (Jump et al., 2009), mountains allowed plant species to track warm interglacials/cold glacials by means of relatively narrow altitudinal shifts instead of much larger latitudinal migrations.

In East Asia, the link between mountains and plant refugia has been acknowledged in recent years, thanks to a growing body of biogeographical studies focused in China and Japan (see the review papers by L pez-Pujol et al., 2011; Ohsawa and Ide, 2011; Qiu et al., 2011; Liu et al., 2012). In the Korean Peninsula, a series of population genetics studies seems to corroborate such a role for its mountain ranges. Using allozymes, M. G. Chung and his collaborators (Chung and Epperson, 1999; Chung et al., 1999, 2001, 2009, 2012, 2013a,b) have found a common pattern of high/moderate within-population and low/moderate between-population genetic variation for a series of species native to the so-called “Baekdudaegan” (the main mountain system of the Peninsula, which runs north to south, 1625 km long; Fig. 1), including both boreal and temperate, widespread and range-restricted species. According to these authors (Chung et al., 2012, 2013a,b), this apparent pattern of genetic diversity might be attributable to the existence of large refugial areas (“macrorefugia” sensu Rull, 2009), through the Baekdudaegan. The varied topography of these mountains (peaking over 1500–2000 m above sea level, a.s.l.), coupled with a north–south orientation, the close proximity to the sea, and the fact that remained totally unglaciated (with the exception of a few peaks such as Mt. Baekdu; Fig. 1) would have allowed plant species to have persisted there throughout the glacial/interglacial cycles mainly due to altitudinal shifts, presumably maintaining large effective population sizes (Kong and Watts, 1993).

Plant congeners usually share life-history traits, in particular the breeding system and the seed dispersal mechanism, due to the “phylogenetic signal” (Losos, 2008). Many authors have recommended that, when genetic diversity is analyzed for a given species, to include at least one congeneric species, as a way to avoid—at least partly—the phylogenetic effects (Karron,

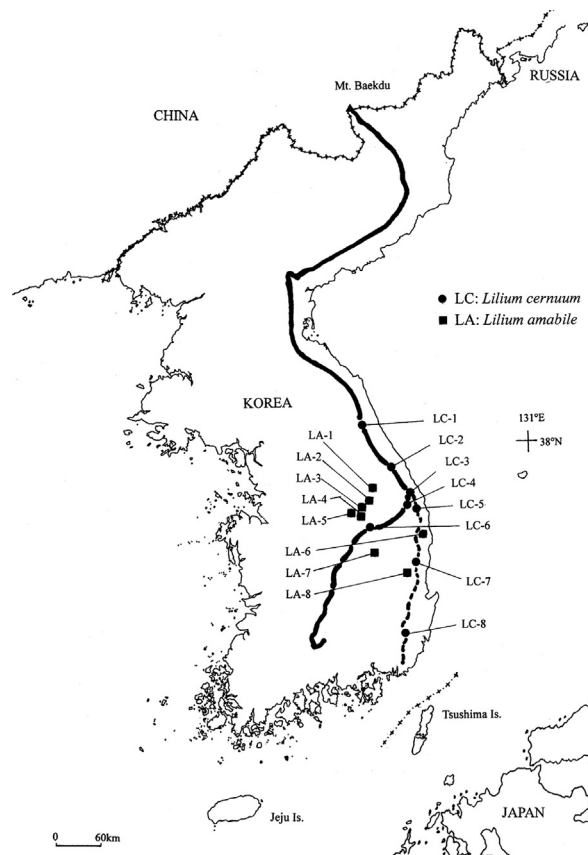


Fig. 1. Locations of sampled populations of *Liliium cernuum* (LC-1 to LC-8) and *L. amabile* (LA-1 to LA-8) in the Korean Peninsula. Solid line indicates the location and shape of the main mountain range of the country, the so-called “Baekdudaegan”, which runs north to south along the Korean Peninsula, and dotted line represents the so-called “Nakdongjeongmaek”, one of the 13 mountainous branches of the Baekdudaegan.

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